

SEQUENCE LISTING

<110> Glucksmann, Maria Alexandra
Silos-Santiago, Inmaculada

<120> Novel Seven-Transmembrane
Proteins/G-Protein Coupled Receptors

<130> 35800/208932

<150> 60/182,061

<151> 2000-02-11

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<211> 1875

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<220>

<221> CDS

<222> (323)...(1522)

<221> misc_feature

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ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 1264
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gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 1312
 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr
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ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 1360
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 Leu Ser Val Ser Ala Ser Pro Ser Val Phe Cys Phe Ser Cys Met Gln
 65 70 75 80

Gly Pro Ile Leu Trp Ile Met Ala Asn Leu Ser Gln Pro Ser Glu Phe
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Val Leu Leu Gly Phe Ser Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr
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Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile
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Ile Ile Val Met Val Ile Ala Asp Thr His Leu His Thr Pro Met Tyr
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Ala Val Pro Arg Met Leu Ser Asp Leu Leu Val Pro His Lys Val Ile
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Thr Phe Thr Gly Cys Met Val Gln Phe Tyr Phe His Phe Ser Leu Gly
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Ser Thr Ser Phe Leu Ile Leu Thr Asp Met Ala Leu Asp Arg Phe Val
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Val Ile Asn His Phe Phe Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser
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Ile Val Thr Thr Val Leu Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys
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cag atc caa aga agt agc ctt agt aat aac cct ctt ttc cag tat aag 498
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ctg cta aca ttg ccc agg cag cat ctg gtt cag ctt tat cta tat ttt 594
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His Asn Asp Ile Cys Ala Ile Cys Tyr Gln Asp Met Lys Ser Ala Val
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atc acg cct tgc agt cat ttt ttc cat gca ggc tgt ctt aag aaa tgg 2034
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Leu Tyr Val Gln Glu Thr Cys Pro Leu Cys His Cys His Leu Lys Asn
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Ser Ser Gln Leu Pro Gly Leu Gly Thr Glu Pro Val Leu Gln Pro His
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Ala Gly Ala Glu Gln Asn Val Met Phe Gln Glu Gly Thr Glu Pro Pro
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ggc cag gag cat act cca ggg acc agg ata cag gaa ggt tcc agg gac 2226
Gly Gln Glu His Thr Pro Gly Thr Arg Ile Gln Glu Gly Ser Arg Asp
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Asn Asn Glu Tyr Ile Ala Arg Arg Pro Asp Asn Gln Glu Gly Ala Phe
630 635 640

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gaa tca gcc tag aggagaagca gcaggaatga tgctttgata ctctggagga 2374
Glu Ser Ala *

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3630

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<211> 663

<212> PRT

<213> Homo sapiens

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Ser	Phe	Phe	Gln	Gln	Ile	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu
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Phe	Gln	Tyr	Lys	Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	Ile
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Tyr	Leu	Tyr	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Tyr	Ala	Gly	His	Gln	Ile
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Ser	Arg	Asp	Tyr	Val	Arg	Ser	Glu	Leu	Glu	Phe	Ala	Tyr	Glu	Gly	Pro
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Val	Pro	Tyr	Asn	Leu	Ala	Lys	Ser	Ala	Tyr	Arg	Glu	Leu	Val	Gln	Val
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His	Arg	Ala	Phe	Leu	Leu	Ser	Ile	Ile	Leu	Phe	Ile	Val	Val	Ala	Ser
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 Cys Gln Phe Phe His Met Asp Phe Trp Leu Leu Ile Ile Ile Ser Ser
 405 410 415
 Ser Ile Leu Thr Ser Leu Gln Val Leu Gly Thr Leu Phe Ile Tyr Val
 420 425 430
 Leu Phe Met Val Glu Glu Phe Arg Lys Glu Pro Val Glu Asn Met Asp
 435 440 445
 Asp Val Ile Tyr Tyr Val Asn Gly Thr Tyr Arg Leu Leu Glu Phe Leu
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 Arg Asp Ala Val Asn Lys Ile Lys Ser Leu Pro Ile Ala Thr Lys Glu
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 Gln Leu Glu Lys His Asn Asp Ile Cys Ala Ile Cys Tyr Gln Asp Met
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 Lys Ser Ala Val Ile Thr Pro Cys Ser His Phe Phe His Ala Gly Cys
 545 550 555 560
 Leu Lys Lys Trp Leu Tyr Val Gln Glu Thr Cys Pro Leu Cys His Cys
 565 570 575
 His Leu Lys Asn Ser Ser Gln Leu Pro Gly Leu Gly Thr Glu Pro Val
 580 585 590
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 595 600 605
 Thr Glu Pro Pro Gly Gln Glu His Thr Pro Gly Thr Arg Ile Gln Glu
 610 615 620
 Gly Ser Arg Asp Asn Asn Glu Tyr Ile Ala Arg Arg Pro Asp Asn Gln
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agg gga aga act gag agg cgc ata ccc cgg ctg tgg cgg ctg ctg ctc 398
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tgg gct ggg acc gcc ttc cag gtg acc cag gga acg gga ccg gag ctt 446
Trp Ala Gly Thr Ala Phe Gln Val Thr Gln Gly Thr Gly Pro Glu Leu
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cac gcc tgc aaa gag tct gag tac cac tat gag tac acg gcg tgt gac 494
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Leu Met Tyr Ala Val Asn Leu Lys Gln Ser Gly Thr Val Asn Phe Glu
180 185 190
Tyr Tyr Tyr Pro Asp Ser Ser Ile Ile Phe Glu Phe Phe Val Gln Asn
195 200 205
Asp Gln Cys Gln Pro Asn Ala Asp Asp Ser Arg Trp Met Lys Thr Thr
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Glu Lys Gly Trp Glu Phe His Ser Val Glu Leu Asn Arg Gly Asn Asn
225 230 235 240
Val Leu Tyr Trp Arg Thr Thr Ala Phe Ser Val Trp Thr Lys Val Pro
245 250 255
Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala Tyr Thr
260 265 270
Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys Gln Gly
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Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn Lys Gly
290 295 300
Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Gly Asp Val
305 310 315 320
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Lys Glu Ile Pro Gly Asn Arg Ala Ile Leu Leu Ala Lys Leu Arg Met
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Ile	Ile	Met	Ser	Ser	Thr	Cys	Glu	Leu	Glu	Arg	Val	Leu	Pro	Thr	Ala
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Leu	Leu	Val	Thr	Leu	Trp	Leu	Ala	Tyr	Val	Asn	Ser	Cys	Leu	Asn	Pro
				245					250					255	
Ile	Ile	Tyr													